



1

SEQUENCE LISTING

<110> ADLER, JON ELLIOT

<120> T2R TASTE RECEPTORS AND GENES ENCODING SAME

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<141> 2001-04-05

<150> 60/195,532

<151> 2000-04-07

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<170> PatentIn Ver. 2.1

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<210> 2

<211> 333

<212> PRT

<213> Homo sapiens

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 Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
 50 55 60
 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
 65 70 75 80
 Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
 85 90 95
 Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
 100 105 110
 Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
 115 120 125
 Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
 130 135 140
 Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
 145 150 155 160
 Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
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 Asn Asn Asn Thr Arg Leu Asn Trp Gln Ile Lys Asp Leu Asn Leu Phe
 180 185 190
 Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
 195 200 205
 Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
 210 215 220
 Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
 225 230 235 240
 Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
 245 250 255
 Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
 260 265 270
 Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
 275 280 285
 Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
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 Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
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 Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val Gln
 35 40 45
 Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
 50 55 60
 Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
 65 70 75 80
 Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
 85 90 95
 Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
 100 105 110
 Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
 115 120 125
 Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
 130 135 140

Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
 145 150 155 160

Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
 165 170 175

Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
 180 185 190

Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
 195 200 205

Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
 210 215 220

Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
 225 230 235 240

Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
 245 250 255

Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
 260 265 270

Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
 275 280 285

Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
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Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
 305 310 315 320

Leu

<210> 5

<211> 972

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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35 40 45

Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
50 55 60

Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
65 70 75 80

Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
85 90 95

Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
100 105 110

Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
115 120 125

Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
130 135 140

Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu
145 150 155 160

Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
165 170 175

Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
180 185 190

Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
195 200 205

Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
210 215 220

Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
225 230 235 240

Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
245 250 255

Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
 260 265 270

Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
 275 280 285

Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
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Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
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Gln Thr Leu

<210> 7
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 gcttgctcatc tttttgtgat aaacatgaat gagattgtgc ggacaaaaga atttgaagga 480
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 <211> 309
 <212> PRT
 <213> Homo sapiens

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 35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Asn Ser Val Glu Val
 65 70 75 80
 Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
 130 135 140
 Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Asn
 165 170 175
 Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Phe Trp Gln Met Arg Tyr Trp Val Lys Gly Glu
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 Lys Thr Ser Ser Pro
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<211> 930

<212> DNA

<213> Homo sapiens

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 atctcctcag ctgatcaaat tattgctgct ctggcagtct ccagagttgg tttgctctgg 180

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<210> 10

<211> 309

<212> PRT

<213> Homo sapiens

<400> 10

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      20           25           30

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Ile Ala Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile
      35           40           45

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Ala Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
      50           55           60

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His Trp Tyr Ser Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val
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Ile Ile Phe Ile Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
      85           90           95

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Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
      100          105          110

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Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
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Val Leu Val Ile Val Leu Gly Ser Leu Phe Phe Leu Val Cys His Leu
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Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Glu Glu Cys Glu Gly
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Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Met His Leu Ser Asn
      165          170          175

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Leu Thr Val Ala Met Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
      180          185          190

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Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Ile His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Ile Leu Leu Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Leu Ile Ile Ser Phe Trp Asn Phe Lys Met Arg Pro
 245 250 255

Lys Glu Ile Val Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro
 260 265 270

Ser Phe His Ser Phe Ile Leu Ile Trp Gly Asn Lys Thr Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Val Thr Cys Trp Ala Lys Gly Gln
 290 295 300

Asn Gln Ser Thr Pro
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<210> 11
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 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60
 Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
 65 70 75 80
 Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
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 115 120 125
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 165 170 175
 Ala Thr Val Thr Thr Leu Gly Asn Leu Val Pro Phe Thr Leu Thr Leu
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 Leu Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Ile Phe Phe Leu Leu Leu Cys Ala Val
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 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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 Thr Phe Leu Ser Val Leu Arg Gln Val Arg Tyr Trp Val Lys Gly Glu
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 Lys Pro Ser Ser Pro
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<210> 14
 <211> 299
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe
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 Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val
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 Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met
 85 90 95
 Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
 130 135 140
 Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln
 245 250 255

Ser Lys Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro
 260 265 270

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 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Met Thr Arg
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<210> 15

<211> 900

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16

<211> 299

<212> PRT

<213> Homo sapiens

<400> 16

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 20 25 30

Ile Asp Trp Val Lys Arg Lys Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu
 50 55 60

Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
 65 70 75 80

Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met
 85 90 95

Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val
 115 120 125

Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu
 130 135 140

Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly
 145 150 155 160

Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr
 165 170 175

Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
 245 250 255

Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
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Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
 275 280 285

Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
 290 295

<210> 17
 <211> 924
 <212> DNA
 <213> Homo sapiens

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<210> 18
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 18
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 Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
 35 40 45
 Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
 50 55 60
 His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
 65 70 75 80
 Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
 85 90 95
 Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile Ala
 100 105 110
 Asn Ile Thr His Ser Thr Phe Leu Trp Leu Lys Trp Arg Phe Pro Gly
 115 120 125
 Trp Val Pro Trp Leu Leu Leu Gly Ser Val Leu Ile Ser Phe Ile Ile
 130 135 140

Thr Leu Leu Phe Phe Trp Val Asn Tyr Pro Val Tyr Gln Glu Phe Leu
145 150 155 160

Ile Arg Lys Phe Ser Gly Asn Met Thr Tyr Lys Trp Asn Thr Arg Ile
165 170 175

Glu Thr Tyr Tyr Phe Pro Ser Leu Lys Leu Val Ile Trp Ser Ile Pro
180 185 190

Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
195 200 205

Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
210 215 220

Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
225 230 235 240

Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
245 250 255

Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
260 265 270

Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
275 280 285

Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe
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Trp Val Ala
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<210> 19

<211> 930

<212> DNA

<213> Homo sapiens

<400> 19

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<210> 20
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 20

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			20					25					30		
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		35					40					45			
Thr	Ala	Leu	Ala	Val	Ser	Arg	Val	Gly	Leu	Leu	Trp	Val	Leu	Val	Leu
	50					55					60				
Asn	Trp	Tyr	Ala	Thr	Glu	Leu	Asn	Pro	Ala	Phe	Asn	Ser	Ile	Glu	Val
65					70					75					80
Arg	Ile	Thr	Ala	Tyr	Asn	Val	Trp	Ala	Val	Ile	Asn	His	Phe	Ser	Asn
				85					90					95	
Trp	Leu	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Ala	Asn
			100					105					110		
Phe	Ser	Asn	Leu	Ile	Phe	Leu	His	Leu	Lys	Arg	Arg	Val	Lys	Ser	Val
		115					120					125			
Val	Leu	Val	Ile	Leu	Leu	Gly	Pro	Leu	Leu	Phe	Leu	Val	Cys	His	Leu
	130					135					140				
Phe	Val	Ile	Asn	Met	Asn	Gln	Ile	Ile	Trp	Thr	Lys	Glu	Tyr	Glu	Gly
145					150					155					160
Asn	Met	Thr	Trp	Lys	Ile	Lys	Leu	Arg	Ser	Ala	Met	Tyr	Leu	Ser	Asn
				165					170					175	
Thr	Thr	Val	Thr	Ile	Leu	Ala	Asn	Leu	Val	Pro	Phe	Thr	Leu	Thr	Leu
			180					185					190		
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		195					200					205			
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	210					215					220				
Ile	Lys	Ala	Leu	Gln	Thr	Val	Thr	Ser	Phe	Leu	Leu	Leu	Cys	Ala	Ile
225					230					235					240
Tyr	Phe	Leu	Ser	Ile	Ile	Met	Ser	Val	Trp	Ser	Phe	Glu	Ser	Leu	Glu
				245					250					255	
Asn	Lys	Pro	Val	Phe	Met	Phe	Cys	Glu	Ala	Ile	Ala	Phe	Ser	Tyr	Pro
			260					265					270		

Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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Lys Pro Ser Ser Ser
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<210> 21
 <211> 930
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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 <211> 912
 <212> DNA
 <213> Mus sp.

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<210> 24
 <211> 303
 <212> PRT
 <213> Mus sp.

<400> 24
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 35 40 45
 Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met
 50 55 60
 Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn
 65 70 75 80
 Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile
 85 90 95
 Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
 100 105 110
 Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser
 115 120 125
 Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly
 130 135 140

Thr	Ala	Thr	Val	Cys	Ile	Glu	Val	Gly	Phe	Pro	Leu	Ile	Glu	Asp	Gly
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Tyr	Val	Leu	Arg	Asn	Ala	Gly	Leu	Asn	Asp	Ser	Asn	Ala	Lys	Leu	Val
				165					170					175	
Arg	Asn	Asn	Asp	Leu	Leu	Leu	Ile	Asn	Leu	Ile	Leu	Leu	Leu	Pro	Leu
			180					185					190		
Ser	Val	Phe	Val	Met	Cys	Thr	Ser	Met	Leu	Phe	Val	Ser	Leu	Tyr	Lys
		195					200					205			
His	Met	His	Trp	Met	Gln	Ser	Glu	Ser	His	Lys	Leu	Ser	Ser	Ala	Arg
	210					215					220				
Thr	Glu	Ala	His	Ile	Asn	Ala	Leu	Lys	Thr	Val	Thr	Thr	Phe	Phe	Cys
225					230					235					240
Phe	Phe	Val	Ser	Tyr	Phe	Ala	Ala	Phe	Met	Ala	Asn	Met	Thr	Phe	Arg
				245					250					255	
Ile	Pro	Tyr	Arg	Ser	His	Gln	Phe	Phe	Val	Val	Lys	Glu	Ile	Met	Ala
			260					265					270		
Ala	Tyr	Pro	Ala	Gly	His	Ser	Val	Ile	Ile	Val	Leu	Ser	Asn	Ser	Lys
		275					280					285			
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<210> 25
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 <212> PRT
 <213> Artificial Sequence

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 <223> Phe or Gly

<220>
 <221> MOD_RES
 <222> (3)
 <223> Ile, Val or Leu

<220>
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 <222> (4)
 <223> Val or Leu

<220>
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 <222> (6)
 <223> Ile or Val

<220>
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<222> (7)
 <223> Leu or Val

<220>
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 <222> (10)
 <223> Gly or Thr

<220>
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 <222> (13)
 <223> Val or Ala

<220>
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 <222> (18)
 <223> Ile or Met

<220>
 <223> Description of Artificial Sequence: Consensus
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<400> 25
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Cys Xaa Asp Trp
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<210> 26
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> Asp or Gly

<220>
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 <222> (2)
 <223> Phe or Leu

<220>
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 <222> (3)
 <223> Ile or Leu

<220>
 <221> MOD_RES
 <222> (5)
 <223> Thr or Ile

<220>
 <221> MOD_RES

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<222> (12)  
<223> Ser, Asn or Gly
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<220>
 <221> MOD_RES
 <222> (13)
 <223> Ile or Val

<220>
 <223> Description of Artificial Sequence: Consensus
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<400> 27
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<210> 28
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> MOD_RES
 <222> (3)
 <223> Phe or Cys

<220>
 <221> MOD_RES
 <222> (8)
 <223> Asn or Ser

<220>
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 <222> (11)
 <223> His or Asn

<220>
 <221> MOD_RES
 <222> (12)
 <223> Pro or Ser

<220>
 <221> MOD_RES
 <222> (13)
 <223> Leu, Ile or Val

<220>
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 <222> (16)
 <223> Trp or Tyr

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 28
 Phe Tyr Xaa Leu Lys Ile Ala Xaa Phe Ser Xaa Xaa Xaa Phe Leu Xaa
 1 5 10 15

Leu Lys

<210> 29
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ile, Phe or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (10)
 <223> Ser or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (12)
 <223> Gln or Lys

<220>
 <221> MOD_RES
 <222> (13)
 <223> Met or Ile

<220>
 <221> MOD_RES
 <222> (14)
 <223> Gln or Lys

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 29
 Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 30
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> MOD_RES
 <222> (3)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ile or Val

<220>
 <221> MOD_RES
 <222> (7)
 <223> Leu or Met

<220>
 <221> MOD_RES
 <222> (8)
 <223> Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (10)
 <223> Pro, Ser or Asn

<220>
 <221> MOD_RES
 <222> (13)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (14)
 <223> Gln or Arg

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 30
 His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa
 1 5 10

<210> 31
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide translocation domain

<400> 31
 Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys
 1 5 10 15

Thr Gly Val Val
 20